

## RAW SEQUENCE LISTING

DATE: 06/14/2001

PATENT APPLICATION: US/09/779,050A

TIME: 13:03:05

Input Set : A:\A-570B.ST25.txt

Output Set: N:\CRF3\06142001\I779050A.raw

ENTERED

See p.5

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3 <110> APPLICANT: BOYLE, WILLIAM
4   HSU, HAILING
6 <120> TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
8 <130> FILE REFERENCE: A-570B
10 <140> CURRENT APPLICATION NUMBER: 09/779,050A
11 <141> CURRENT FILING DATE: 2001-02-12
13 <150> PRIOR APPLICATION NUMBER: 60/181,800
14 <151> PRIOR FILING DATE: 2000-02-11
16 <160> NUMBER OF SEQ ID NOS: 52
18 <170> SOFTWARE: PatentIn version 3.0
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21 <211> LENGTH: 1173
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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26 <221> NAME/KEY: CDS
27 <222> LOCATION: (143)..(997)
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32 acaaacacag ataacaggaa atgatccatt ccctgtggtc acttattcta aaggccccaa      120
34 ccttcaaagt tcaagtagtg at atg gat gac tcc aca gaa agg gag cag tca      172
35                               Met Asp Asp Ser Thr Glu Arg Glu Gln Ser
36                               1               5               10
38 cgc ctt act tct tgc ctt aag aaa aga gaa gaa atg aaa ctg aag gag      220
39 Arg Leu Thr Ser Cys Leu Lys Lys Arg Glu Glu Met Lys Leu Lys Glu
40                               15               20               25
42 tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct gtc cga tcc tcc      268
43 Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser Ser
44                               30               35               40
46 aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg gca ctg ctg tct      316
47 Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser
48                               45               50               55
50 tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc gcc ctg caa ggg      364
51 Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly
52                               60               65               70
54 gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac cac gcg gag aag      412
55 Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu Lys
56 75                               80               85               90
58 ctg cca gca gga gca gga gcc ccc aag gcc gcc ctg gag gaa gct cca      460
59 Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro
60                               95               100              105
62 gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca gct cca gga gaa      508
63 Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu
64                               110              115              120
66 ggc aac tcc agt cag aac agc aga aat aag cgt gcc gtt cag ggt cca      556
67 Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala Val Gln Gly Pro
68                               125              130              135

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70 gaa gaa aca gtc act caa gac tgc ttg caa ctg att gca gac agt gaa      604
71 Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu
72      140                      145                      150
74 aca cca act ata caa aaa gga tct tac aca ttt gtt cca tgg ctt ctc      652
75 Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu
76 155                      160                      165                      170
78 agc ttt aaa agg gga agt gcc cta gaa gaa aaa gag aat aaa ata ttg      700
79 Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu
80                      175                      180                      185
82 gtc aaa gaa act ggt tac ttt ttt ata tat ggt cag gtt tta tat act      748
83 Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr
84                      190                      195                      200
86 gat aag acc tac gcc atg gga cat cta att cag agg aag aag gtc cat      796
87 Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg Lys Lys Val His
88      205                      210                      215
90 gtc ttt ggg gat gaa ttg agt ctg gtg act ttg ttt cga tgt att caa      844
91 Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln
92      220                      225                      230
94 aat atg cct gaa aca cta ccc aat aat tcc tgc tat tca gct ggc att      892
95 Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile
96 235                      240                      245                      250
98 gca aaa ctg gaa gaa gga gat gaa ctc caa ctt gca ata cca aga gaa      940
99 Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu
100                      255                      260                      265
102 aat gca caa ata tca ctg gat gga gat gtc aca ttt ttt ggt gca ttg      988
103 Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr Phe Phe Gly Ala Leu
104                      270                      275                      280
106 aaa ctg ctg tgacctactt acaccatgtc tgtagctatt ttcctccctt      1037
107 Lys Leu Leu
108      285
110 tctctgtacc tctaagaaga aagaatctaa ctgaaaatac caaaaaaaaa aaaaaaaaaa      1097
112 aaaaaaaaaagt agttaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1157
114 aaaaactcgg aggggg      1173
117 <210> SEQ ID NO: 2
118 <211> LENGTH: 285
119 <212> TYPE: PRT
120 <213> ORGANISM: Homo sapiens
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125 1                      5                      10                      15
128 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
129      20                      25                      30
132 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
133      35                      40                      45
136 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
137      50                      55                      60
140 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
141 65                      70                      75                      80
144 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly

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145          85          90          95
148 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
149          100          105          110
152 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
153          115          120          125
156 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
157          130          135          140
160 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
161 145          150          155          160
164 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
165          165          170          175
168 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
169          180          185          190
172 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
173          195          200          205
176 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
177          210          215          220
180 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
181 225          230          235          240
184 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
185          245          250          255
188 Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
189          260          265          270
192 Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
193          275          280          285
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197 <211> LENGTH: 1139
198 <212> TYPE: DNA
199 <213> ORGANISM: Mus musculus
201 <220> FEATURE:
202 <221> NAME/KEY: CDS
203 <222> LOCATION: (52)..(978)
205 <400> SEQUENCE: 3
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207                               Met Asp
208                               1
210 gag tct gca aag acc ctg cca cca ccg tgc ctc tgt ttt tgc tcc gag 105
211 Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys Ser Glu
212          5          10          15
214 aaa gga gaa gat atg aaa gtg gga tat gat ccc atc act ccg cag aag 153
215 Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro Gln Lys
216          20          25          30
218 gag gag ggt gcc tgg ttt ggg atc tgc agg gat gga agg ctg ctg gct 201
219 Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu Leu Ala
220 35          40          45          50
222 gct acc ctc ctg ctg gcc ctg ttg tcc agc agt ttc aca gcg atg tcc 249
223 Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala Met Ser
224          55          60          65
226 ttg tac cag ttg gct gcc ttg caa gca gac ctg atg aac ctg cgc atg 297

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227 Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu Arg Met
228      70      75      80
230 gag ctg cag agc tac cga ggt tca gca aca cca gcc gcc gcg ggt gct      345
231 Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala Gly Ala
232      85      90      95
234 cca gag ttg acc gct gga gtc aaa ctc ctg aca ccg gca gct cct cga      393
235 Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala Pro Arg
236      100      105      110
238 ccc cac aac tcc agc cgc ggc cac agg aac aga cgc gct ttc cag gga      441
239 Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe Gln Gly
240 115      120      125      130
242 cca gag gaa aca gaa caa gat gta gac ctc tca gct cct cct gca cca      489
243 Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro Ala Pro
244      135      140      145
246 tgc ctg cct gga tgc cgc cat tct caa cat gat gat aat gga atg aac      537
247 Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly Met Asn
248      150      155      160
250 ctc aga aac atc att caa gac tgt ctg cag ctg att gca gac agc gac      585
251 Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser Asp
252      165      170      175
254 acg ccg act ata cga aaa gga act tac aca ttt gtt cca tgg ctt ctc      633
255 Thr Pro Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp Leu Leu
256      180      185      190
258 agc ttt aaa aga gga aat gcc ttg gag gag aaa gag aac aaa ata gtg      681
259 Ser Phe Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys Ile Val
260 195      200      205      210
262 gtg agg caa aca ggc tat ttc ttc atc tac agc cag gtt cta tac acg      729
263 Val Arg Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu Tyr Thr
264      215      220      225
266 gac ccc atc ttt gct atg ggt cat gtc atc cag agg aag aaa gta cac      777
267 Asp Pro Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys Val His
268      230      235      240
270 gtc ttt ggg gac gag ctg agc ctg gtg acc ctg ttc cga tgt att cag      825
271 Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln
272      245      250      255
274 aat atg ccc aaa aca ctg ccc aac aat tcc tgc tac ttg gct ggc atc      873
275 Asn Met Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Leu Ala Gly Ile
276      260      265      270
278 gcg agg ctg gaa gaa gga gat gag att cag ctt gca att cct cgg gag      921
279 Ala Arg Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro Arg Glu
280 275      280      285      290
282 aat gca cag att tca cgc aac gga gac gac acc ttc ttt ggt gcc cta      969
283 Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly Ala Leu
284      295      300      305
286 aaa ctg ctg' taactcactt gctggagtgc gtgatcccct tccctcgtct      1018
287 Lys Leu Leu
290 tctctgtacc tccgagggag aaacagacga ctggaaaaat aaaagatggg gaaagccgtc      1078
292 agcgaaagtt ttctcgtgac ccgttgaatc tgatccaaac caggaaatat aacagacagc      1138
294 c      1139

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297 <210> SEQ ID NO: 4
298 <211> LENGTH: 309
299 <212> TYPE: PRT
300 <213> ORGANISM: Mus musculus
302 <400> SEQUENCE: 4
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305 1 5 10 15
308 Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
309 20 25 30
312 Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
313 35 40 45
316 Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
317 50 55 60
320 Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
321 65 70 75 80
324 Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
325 85 90 95
328 Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
329 100 105 110
332 Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
333 115 120 125
336 Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
337 130 135 140
340 Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
341 145 150 155 160
344 Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
345 165 170 175
348 Ser Asp Thr Pro Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp
349 180 185 190
352 Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys
353 195 200 205
356 Ile Val Val Arg Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu
357 210 215 220
360 Tyr Thr Asp Pro Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys
361 225 230 235 240
364 Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys
365 245 250 255
368 Ile Gln Asn Met Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Leu Ala
369 260 265 270
372 Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro
373 275 280 285
376 Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly
377 290 295 300
380 Ala Leu Lys Leu Leu
381 305
384 <210> SEQ ID NO: 5
385 <211> LENGTH: 278
386 <212> TYPE: PRT
387 <213> ORGANISM: Homo sapiens

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

DATE: 06/14/2001

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Input Set : A:\A-570B.ST25.txt

Output Set: N:\CRF3\06142001\I779050A.raw

L:398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:416 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:425 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:431 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:434 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:440 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:474 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:1146 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25  
L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:1168 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26  
L:1181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:1190 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27  
L:1203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27